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TECH CENTER 1600/2900

SEQUENCE LISTING

<110> McKeon, F.  
Kayako, K.  
Ryeom, S.

<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN  
USES AND REAGENTS RELATED THERETO

<130> HMV-048.01

<140> 09/575,580

<141> 2000-05-22

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
 50 55 60  
 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu  
 65 70 75 80  
 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu  
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 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser  
 100 105 110  
 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn  
 115 120 125  
 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr  
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 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg  
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 Leu Thr Asp Phe Ser Asp Leu Pro Asn Ser Leu Phe Ala Cys Asn Val  
 50 55 60

His Gln Ser Val Phe Glu Glu Glu Glu Ser Lys Glu Lys Phe Glu Gly  
 65 70 75 80  
 Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe Lys Ser  
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 Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala Ala Arg  
 100 105 110  
 Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Pro  
 115 120 125  
 Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu  
 130 135 140  
 His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro  
 145 150 155 160  
 Ser Ser Pro Ser Val Gly Trp Lys Pro Ile Ser Asp Ala Thr Pro Val  
 165 170 175  
 Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu  
 180 185 190  
 Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val  
 195 200 205  
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 <212> PRT  
 <213> Homo sapiens

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 Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile  
 50 55 60  
 Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe  
 65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala  
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro  
100 105 110

Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr  
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu  
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Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys  
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Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro  
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Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn  
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<211> 170

<212> PRT

<213> Homo sapiens

<400> 7

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Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr  
35 40 45

Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His  
50 55 60

Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu  
65 70 75 80

Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp  
85 90 95

Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu  
100 105 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro  
115 120 125

Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu

B2  
cont.

130

135

140

Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr  
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Arg Arg Pro Glu Tyr Thr Pro Ile His Leu  
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&lt;210&gt; 8

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Cricetulus griseus

&lt;400&gt; 8

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Val Ala Asn Gly Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe  
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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe  
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu  
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu  
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser  
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn  
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr  
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val  
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg Met  
165 170 175

Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr  
180 185 190

Pro Ile His Leu Ser  
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&lt;210&gt; 9

&lt;211&gt; 207

<212> PRT

<213> *Caenorhabditis elegans*

<400> 9

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| Met | Val | Ala | Asp | Asn | Ser | Glu | Lys | Ser | Thr | Lys | Ser | Val | Ala | Asn | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Leu | Ile | Ser | Thr | Val | Ser | Ser | Lys | Asp | Asp | Leu | Pro | Asn | Ala | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Val | Thr | Gln | Val | Pro | Glu | Asp | Val | Phe | Asp | Asn | Lys | Gln | Asp | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Asn | Phe | Ser | Ser | Leu | Phe | Thr | Gln | Ile | Glu | Lys | Asp | Ile | His | Phe |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Phe | Leu | Arg | Ser | Phe | Arg | Arg | Val | Arg | Val | Ile | Phe | Ser | Ser | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Asn | Ala | Thr | Ala | Ala | Lys | Leu | Ile | Val | Gln | Gly | Phe | Ser | Phe | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |
| Gly | His | Glu | Leu | Lys | Ala | Phe | Phe | Ala | Gln | Arg | Ile | Tyr | Met | Ser | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Ser | Gln | Met | Leu | Ser | Pro | Pro | Pro | Leu | Glu | Lys | Gln | Phe | Leu | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Pro | Pro | Cys | Ser | Pro | Pro | Val | Gly | Trp | Glu | Gln | Thr | Lys | Asp | Met |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Pro | Val | Val | Cys | Asn | Phe | Asp | Leu | Met | Ala | Arg | Leu | Ala | Ser | Phe |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Ile | Asp | Glu | Lys | Tyr | Glu | Val | His | Asn | Gly | Asp | Glu | Leu | Thr | Pro |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Ile | Ile | Val | His | Pro | Cys | Glu | Thr | Pro | Ile | Asp | Val | Pro | Ser | Ala |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile | Glu | Met | Pro | Arg | Thr | Pro | Arg | Pro | Ser | Ser | Pro | Cys | Glu | Gln |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |

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<211> 211

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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| Met | Gly | Asn | Ile | Ile | Thr | Asp | Thr | Ile | Ile | Ile | Thr | Ser | Asp | Lys | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Ile | Val | Asp | Asn | Asp | Asn | Val | Glu | Arg | Ile | Gln | Val | Trp | Leu | Ser |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Asn | Ile | Leu | Arg | Lys | Phe | Gln | Ile | Asn | Glu | Asn | Glu | Pro | Leu | Gln |  |

35

40

45

Leu Ile Ile Leu Lys Arg Phe Lys Arg Ile Leu Leu Ile Cys Pro Ser  
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 Glu Asn Phe Asn Phe Ser Tyr Ser Leu Gln Asp Gly Gln Arg Asn Leu  
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 Ser Pro Pro Ala Ser Pro Pro Pro Glu Phe Asp Phe Ser Lys Cys Glu  
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 165 170 175  
 Ile Asp Arg Cys Pro Thr Asn Asp Gly Asn Gly Gln Met Gln Leu Ala  
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 Asp Asp Asp  
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&lt;210&gt; 11

&lt;211&gt; 163

&lt;212&gt; PRT

&lt;213&gt; Schizosaccharomyces pombe

&lt;400&gt; 11

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 Leu Gly Lys Val Leu Ala Ser Tyr Asn Asp Lys Ala Val Glu Glu Asp  
 35 40 45  
 Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val  
 50 55 60  
 His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser  
 65 70 75 80



Val Asp Gln Ser Leu Gln Val Pro Lys Phe Glu Lys Asn Trp Leu Ile  
85 90 95

Ser Pro Pro Gly Ser Pro Pro Val Gly Trp Glu Pro Ile Val Glu Glu  
100 105 110

Ser Pro Asn Ser Gln His Leu Ala His Asp Ile Gln Leu Lys Leu Asp  
115 120 125

Glu Leu Gly Asn Ala Leu Leu Asn Asp His Ser Ala Gly Pro Gln Ile  
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Phe Glu His

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<213> Homo sapiens

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<212> DNA

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<210> 24

<211> 236

<212> PRT

<213> Mus musculus

<400> 24

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|---|-----|-----|-----|
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| Cys Ser Ser Asp Gln Glu Glu Glu Glu Glu Met Val Phe Gly Glu Asn |     |     |     |
| 20  |     | 25  | 30  |
| Glu Asp Gly Leu Glu Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser |     |     |     |
| 35  | 40  | 45  |     |
| Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Val Gln Glu Gln |     |     |     |
| 50  | 55  | 60  |     |
| Lys Glu Arg Phe Glu Ala Leu Phe Thr Leu Tyr Asp Asp Gln Val Thr |     |     |     |
| 65  | 70  | 75  | 80  |
| Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys |     |     |     |
| 85  | 90  | 95  |     |
| Pro Ala Arg Ala Arg Ile Glu Leu His Glu Ser Glu Phe His Gly Arg |     |     |     |
| 100   | 105 | 110 |     |
| Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Val Ser Gly Glu Ala Arg |     |     |     |
| 115   | 120 | 125 |     |
| Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Thr Lys Gln Phe Leu Ile |     |     |     |
| 130   | 135 | 140 |     |
| Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser Glu Asp Ala |     |     |     |
| 145   | 150 | 155 | 160 |
| Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser Lys Leu Gly |     |     |     |
| 165   | 170 | 175 |     |
| Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser |     |     |     |
| 180   | 185 | 190 |     |
| Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu Glu Asp Thr |     |     |     |
| 195   | 200 | 205 |     |
| Lys Asn Pro Lys Gln Lys Ile Thr Gln Thr Arg Arg Pro Glu Ala Pro |     |     |     |
| 210   | 215 | 220 |     |
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<210> 25

<211> 3983

<212> DNA

<213> Mus musculus

<400> 25

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| tgccccctc   | cctgcacact  | agtcagcttc  | actgggacta  | ggccagcgac  | ctgtcaagag  | 480  |
| ctgtctcaag  | ccagtgcagg  | ttctccacgc  | ctcaccttgt  | aagcctgtat  | tcagatcagc  | 540  |
| acagggctgt  | cagtcggggc  | aggggtgagg  | gtcatcacat  | ggttgagact  | cttagctgag  | 600  |
| gggcagaaaa  | gggggctgtg  | gatgagttgt  | ccattgttct  | gccaacctcg  | gggacacctt  | 660  |
| caaggcgact  | cccaacttcc  | atgtgactgt  | aacggggact  | ggtagatcgc  | agcttctcgt  | 720  |
| tgttatcccc  | aaggtaatgt  | cagtccttgc  | caggctctga  | agccgcttcc  | tttcttctca  | 780  |
| gttgtctaca  | ctcacttcc   | gccagcttag  | ggccagcgga  | gtcctgtgga  | gtgtgggtca  | 840  |
| tggccctcac  | ctctcggtaa  | tggtagattt  | tgaccatgaa  | ataccctctg  | tggctcatgt  | 900  |
| atttgaatac  | ttgggtcctc  | tgtggtgcag  | ttttacagtt  | agggaaacttt | aggaggtggg  | 960  |
| gcctccctaa  | aggaatgaga  | tccccgaggc  | agactctgag  | gggttagagc  | ccagccctt   | 1020 |
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| cacttgaaaa  | gtttacccaa  | cacaggcacc  | aatccggaa   | ttcagtcctt  | ccttcacctc  | 1260 |
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| tgcataatga  | tgaactcatt  | tctctcctca  | gactttacac  | ataggaagtt  | cacacctggc  | 1440 |
| tccgccccat  | cccgacaaac  | agttcctcat  | ctccccctcg  | gcctctcctc  | ccgttggtcg  | 1500 |
| gaaacaagta  | gaagatgcca  | cccccgctcat | aaattacgat  | cttttatatg  | ccatctccaa  | 1560 |
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| tccacattgc  | tgcagctcgt  | gctggagtgt  | gtgccccttg  | gaggattcca  | ggagatggta  | 1740 |
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| acccagcagg  | cacacctgtg  | tggctcactc  | caggccccag  | atcatgttgt  | tccaggtggg  | 1860 |
| atgggaaaag  | gcaaacagtc  | caacctgtag  | ggagtctcgt  | caactgtcat  | tcctacttcc  | 1920 |
| gtactgggtg  | ggagggatgt  | gcgcactctc  | caccccacac  | agcaagccga  | atcagcactg  | 1980 |
| cccatcagcc  | cctcgtcatc  | tgaagttcct  | ttagggcaag  | ggttttat    | tcattggtca  | 2040 |
| tcagcagaaa  | gattacattt  | ctgagaacac  | agcctaaatg  | gaaattcctc  | ccgtgggtaca | 2100 |
| aactgagact  | cacgttacta  | gtgctaattg  | tagcatgaag  | gtcaaaagtg  | gaaacggcca  | 2160 |
| gtgtgagcaa  | ggagacgggt  | cagcatggcg  | gctctcagca  | cagttgaggg  | gtctgttgc   | 2220 |
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| gaaacattcc  | taccagggcc  | atgacagagt  | tctccagacc  | cagagccagc  | acacttcagt  | 2400 |
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| tatagaaaacg | ccccctccac  | ttacagtttt  | cccagcagcc  | ctcaagactt  | ggggagagcc  | 2580 |
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| ccgctacagc  | agctggaaac  | ttagccggtt  | taacaacagg  | gctcaaacc   | gggccttgca  | 2760 |
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| acaaagaagt  | gagacagccc  | ggggacaagt  | cctcatccac  | tcactcccca  | ccatacacgg  | 3000 |
| ccactccgcc  | atgccacctc  | ccctcagtgt  | ctagtgcaga  | ccccctcaag  | ggaaatccca  | 3060 |
| gacccttct   | ttccagccag  | gtttcttggt  | gacagaaggc  | ccatccta    | cttgctatgc  | 3120 |
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| aatataaaac  | caagggaaagg | atgttaaggt  | tgagcagatt  | cacctggggc  | tctctgctgc  | 3480 |
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|            |            |            |            |            |            |      |
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| accactccca | gtgtgggtgg | ccacgtgtgt | gagagtgacc | aagagaatga | ggaggaagag | 3900 |
| gaagagatgg | agagaatgaa | gagacccaag | cccaaaatca | tccagacacg | gagaccgagt | 3960 |
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<210> 26

<211> 3360

<212> DNA

<213> Mus musculus

<400> 26

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| agtttccgac  | gggttcgaat  | aaatttcagc  | catcccaa   | ctgcagcccg  | tgccccgat   | 120  |
| agagcttcat  | gagctcagtt  | cagaggaag   | aagctaaaac | tctacttcgc  | ccaggtgagt  | 180  |
| ctttaacctg  | ctggtttggc  | acaacattta  | gaggacgtgt | tgctattgga  | gtagaatcag  | 240  |
| attcaatttc  | cagcatgcac  | atgggtgggtc | acaaacatct | ggtgccctcc  | tctgacctt   | 300  |
| tagggtacca  | cacacacaca  | cacacacaca  | cacacacaca | cacacacaca  | catacacaca  | 360  |
| cagtacatac  | acataagtgt  | gggcaataca  | ttcatgcaca | taaattaaat  | ttagaagtat  | 420  |
| aaaaagtcac  | tgtaattgg   | aaaataaata  | aattaaatta | aaatgtaaat  | gaggacctcg  | 480  |
| ggagatgggt  | atgcagttaa  | gaaagctggc  | tgctcttcta | gaggacatga  | gttcgagtcc  | 540  |
| tagcactcat  | atgggtgtctc | ataattgttt  | gtaaccctcg | ttacagggga  | accaatgcct  | 600  |
| tcttctagcc  | tcctacacac  | ccacaaatag  | gtttgtgtgt | acagttactt  | cactaagaaa  | 660  |
| ttaatttagt  | ggttgtctaa  | gacctgcccc  | agataaacca | gtcaacattc  | tagcatggag  | 720  |
| agaaaagggg  | gacctgagc   | ccagacctcc  | aactgagggg | ctttcaacag  | ttgatggatg  | 780  |
| cttggggggg  | gggatgtttc  | cttgggtggt  | tggtctctgg | taggttgagt  | atgggtccagg | 840  |
| ggatgggtccc | acacccatgc  | tcactctggac | agcactaact | ggactcagcg  | gatatgaaaa  | 900  |
| cataaagaac  | acgaggaagg  | gaaaggaatg  | gaagcaaata | tgatcaaaat  | atattttatac | 960  |
| atgtatgaaa  | tcctccgagc  | tatttatata  | tgatgaaaat | cctctgagct  | aatgttctta  | 1020 |
| aaataaggaa  | agaaacagac  | actgacagtg  | agttccagat | tgagcagtat  | ctgtgtccta  | 1080 |
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| gctgtgatgg  | tgacatggaa  | agctgtgtgc  | agctgtgcct | agatttctgg  | taaagggaca  | 1260 |
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| aatcttagat  | catcatttat  | taaaacctgc  | atcagaacta | gttgtgtcag  | ctgtagactc  | 1680 |
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| cctgagctat  | ccagtaagggt | cctgtctcaa  | aaagactgtg | tgtgtgtgtg  | tgtgtgtgtg  | 1860 |
| tgtgtgtgtg  | tgtgtgtgtg  | tgtgtgtgtg  | tttaatatgt | gtgtgtgtgt  | gtgtttaata  | 1920 |
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| agacacatac  | atagatacat  | acatagctat  | atagatacga | gagagagaca  | gagagagaga  | 2040 |
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| aaaatcatga  | actcaaacaa  | atagttaagc  | aagaattcac | agcagcactg  | ttcacaatag  | 2160 |
| gccaacagtg  | agaactacct  | aaagatcttc  | aacagataaa | gggataaaga  | gacaatagta  | 2220 |
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| atcaccaaat  | aatgggcctt  | taaaatgcaa  | tggaagctag | acacaaaagc  | tcactgtgtc  | 2340 |
| tgtggttcca  | ttctcataaa  | agagttagat  | aagttcagag | aagtagacac  | agcttgacaa  | 2400 |
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| atcccagcaa  | ccatatgggtg | gctcacaacc  | atccataatg | agatctgatg  | cccttttctg  | 2580 |
| gagtgtctgg  | agacagctac  | catgtactca  | catataataa | ataaataaat  | cttttttaaaa | 2640 |
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| tttgaaaagg  | ccagacccca | gagacagatg | gagacaaact | gcatttgga  | cctccacagc  | 3240 |
| ctgccaaaaca | gttcctcatc | tcacccctt  | catctccatc | tggtggctgg | aagcctatca  | 3300 |
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<213> Mus musculus

<220>

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<222> (1)..(3717)

<223> n=a, c, g, or t

<400> 27

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| ttaagcctct  | gttcatgttt  | ctctgagacg  | aacacctaag  | gggttcattt  | ttctggcgat  | 240  |
| tttgctcagc  | tagggctctg  | tgaggggaagt | cctgatactt  | cgaagtggc   | agattaaaca  | 300  |
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| aaaggtcatc  | aagatggccc  | agggggtgaa  | ggtgcttgcc  | accaagcctg  | gcagcccgag  | 420  |
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| ttccccacat  | tggtcactaa  | gaaaacttcc  | tgctgagcgt  | caggtcttct  | ggagacattt  | 1020 |
| tctcagttgg  | gttcctgtct  | cttgatgact  | aaagcttgca  | tcaggttgac  | atatagtagc  | 1080 |
| cagcacacccc | actcacacca  | ctagcaaata  | cctgggagag  | tcagctgtaa  | aggagaaaag  | 1140 |
| tctcggtttg  | tggtttgag   | gtttcagctc  | gcatgtgatt  | ggcacttttc  | ctgtgagcct  | 1200 |
| gctgtgcagt  | agcacatagg  | ggcagagcaa  | agctcttcac  | ttcgttcatg  | ggaagcagga  | 1260 |
| agagtaaggg  | gttgggggtc  | cactgtccct  | tagggatagt  | ccccatgact  | aaaggcctcc  | 1320 |
| ctgcctcctg  | aaggctccca  | gtttgacctc  | tcagggggagc | aagcctctat  | ttactatgta  | 1380 |
| gagcccaagg  | gtcacttaga  | gccagacca   | cagagtagca  | cgtttatcaa  | gggtccaggg  | 1440 |
| cctgtggcca  | cttccagtc   | accacctgga  | aggtcacaga  | cagtttgaga  | gacagtttta  | 1500 |
| atcacccctc  | caagaaagta  | acaattacca  | taaagtggga  | aatgaaagcc  | ctgtgggtgat | 1560 |
| ggtgcaggcc  | tttaatctaa  | gaactggagg  | cagagaccgt  | gagatctgtg  | agtcaggcct  | 1620 |
| acagagtgag  | ttccaggaca  | gccagggata  | cacggagaaa  | ccctgtctca  | gaaaaagaaa  | 1680 |
| agaaaggaca  | gctgctcaca  | agcacgcctt  | tccctgcagg  | tgcagggtgtc | cggggaggcc  | 1740 |
| cgggacaagt  | cctacttact  | gccaccacag  | cccaccaagc  | agttcctcat  | ctccctccc   | 1800 |
| gcctcacc    | ccgtgggggtg | gaagcagagt  | gaagatgcaa  | tgccagtgat  | caactatgac  | 1860 |
| ctgctctgcg  | ctgtctccaa  | gctggggcca  | ggtactgcat  | tccaccttcg  | ctctccgcgt  | 1920 |
| cctcggacat  | tgtgtttctg  | tgtgttgag   | actgtgtgca  | gtatgggggtg | cagagcccag  | 1980 |

|            |             |            |             |            |             |      |
|------------|-------------|------------|-------------|------------|-------------|------|
| caacaccagc | accgtccagt  | gggcggtgtg | gccacaccag  | tctgagttca | cactcgagct  | 2040 |
| gtacactttc | cagtgtctgtg | gtcctcagcc | agttgcctag  | cctgggttat | ctgagtggtg  | 2100 |
| tctaaggatt | aaacgctgtc  | tgacgctga  | taacttttagc | cattcagcca | gaagttaata  | 2160 |
| taggcgggta | gtgaacatcc  | tactgcttt  | ctctctgcaa  | gccagtcagc | acagtgtctg  | 2220 |
| tcgtttggca | gctgctttgg  | gtgacagtga | caatgacctta | tcgcccttcc | aaagttctat  | 2280 |
| ctctctctct | tttcaacttct | tacttccttc | ttttcttgc   | cggctctact | catctttaat  | 2340 |
| actgcaagaa | gccgattctt  | ctagggcact | tcagaggctt  | ttgagaaggc | actctatgct  | 2400 |
| cctgggcggn | tgagctcttc  | gatggcagag | gccctaccgt  | agacaccgct | gcctagagct  | 2460 |
| tagccagtgc | ctcccatggc  | gccccaacac | caactgtgaat | ttactatcc  | caccttagtt  | 2520 |
| atctatagaa | cagcagttag  | catttatatt | aacatttttaa | ttagtattta | tgtaatataa  | 2580 |
| tcaatgggtt | ctcgtcttct  | tcctgagcac | aaagccagag  | taagcataga | acagaagaga  | 2640 |
| caagaagaga | agagatagga  | agagacagga | gctgtttgca  | aagcaagccc | tccccgagtg  | 2700 |
| aaggaagctg | tgtatattca  | tacagtggca | tgtgcactcc  | tgagcacgcg | cagttgaaaa  | 2760 |
| tcatggagat | gaacatggtg  | gacagggtgt | gcttgggttc  | gcttgacca  | tgaagtttca  | 2820 |
| cttgaataa  | agagaaggat  | ggttttaagg | tgtgtgctaa  | caggagtctg | ccttgaagg   | 2880 |
| gcctgaagt  | cttgattta   | actcctaggg | ctcaggacag  | aagggacggt | gtctttattt  | 2940 |
| atTTTTTTTT | aagacttatg  | tatatgagta | cattgtagct  | gtacagatgg | ctgtgagcct  | 3000 |
| tcattgtggt | gggaattgaa  | tttttaggac | ctttgcttgc  | tcccatcaac | ccctctcgct  | 3060 |
| ctggctggcc | ctgctcgta   | gtccctgctt | gtccagccc   | aaagatttat | ttattattat  | 3120 |
| atataagtac | actgtagctg  | acttcagacg | taccagaaga  | ggacatcaga | tctcattgctg | 3180 |
| ggtagttgtg | agccactatg  | tggttgctgg | gatttgaact  | cttcggaaga | gcatcaagt   | 3240 |
| ttcttactca | ctgagccatc  | gcattagccc | gacagtgtct  | ttacaaatag | aatttctgca  | 3300 |
| gggcatggtg | gtactcaact  | ttaacagcac | ttgggaggca  | gaggctggca | gctccctggg  | 3360 |
| agttccaggt | cagcctgtct  | acacagtgtg | cctaggccag  | cctgggctac | atagtgcgac  | 3420 |
| tccagggagt | ttttgtttt   | gtttttgtt  | tttttaaagt  | ccagcacttg | ggagatggaa  | 3480 |
| gcagaagaat | tagagttcaa  | ggtcagcctc | agctacagca  | gcaagtttct | aactggccca  | 3540 |
| gatttcatga | gacgcagtct  | taaaaaaaaa | aaaaaaaaaat | cagccactga | atgacgtagt  | 3600 |
| agaagaggaa | gttgggagat  | agaagaactt | gatttccttc  | actgggagta | aggctccttc  | 3660 |
| ctgtgcttgc | aggggagaaa  | tacgaactgc | acgcgggaac  | cgagtcacc  | cccagta     | 3717 |

<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: general structure

<220>

<221> SITE

<222> (6)

<223> Xaa=any amino acid residue

<400> 28

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Pro | Lys | Ile | Xaa | Gln | Thr | Arg | Arg | Pro | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: calcineurin



antagonist

<400> 29

Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu  
1 5 10

<210> 30

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: calcineurin  
antagonist

<400> 30

Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly  
1 5 10

<210> 31

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-derived  
peptide

<400> 31

Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys  
1 5 10

<210> 32

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-derived  
peptide

<400> 32

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
1 5 10

<210> 33

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pH-dependent  
membrane-binding internalizing peptide

<220>

<221> SITE

<222> (1)

<223> Xaa=preferably a unique residue, such as Cys or Lys, that facilitates chemical conjugation of the internalizing peptide to a targeting protein conjugate

<220>

<221> SITE

<222> (2)..(3)

<223> Xaa=residues selected to modulate the affinity of the internalizing peptide for different membranes

<400> 33

Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala  
1 5 10 15

Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala  
20 25 30

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide substrate

<400> 34

Gly Asn Ala Ala Ala Ala Arg Arg  
1 5

<210> 35

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (4)..(75)

<220>

<223> Description of Artificial Sequence: synthetic construct

<400> 35

cat atg ggt ggc tgc cgt ggc gat atg ttc ggt tgc ggt gct cct cca 48  
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro  
1 5 10 15

aaa aag aag aga aag gta gct gga ttc  
 Lys Lys Lys Arg Lys Val Ala Gly Phe  
 20

75

<210> 36  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: synthetic  
 construct

<400> 36  
 Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys  
 1 5 10 15  
 Lys Lys Arg Lys Val Ala Gly Phe  
 20

<210> 37  
 <211> 225  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic  
 construct

<220>  
 <221> CDS  
 <222> (4)..(225)

<400> 37  
 cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly  
 1 5 10 15  
 agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96  
 Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys  
 20 25 30  
 ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144  
 Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr  
 35 40 45  
 ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192  
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln  
 50 55 60  
 act cat caa gtt tct cta agt aag caa gga ttc 225  
 Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe  
 65 70

<210> 38  
 <211> 74  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: synthetic  
 construct

<400> 38  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 1 5 10 15  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 20 25 30  
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
 35 40 45  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 50 55 60  
 His Gln Val Ser Leu Ser Lys Gln Gly Phe  
 65 70

<210> 39  
 <211> 912  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic  
 construct

<220>  
 <221> CDS  
 <222> (4)..(912)

<400> 39  
 cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cgg gag gtt ccg 48  
 Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro 15  
 1 5 10 15  
 cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg gcg 96  
 Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala 30  
 20 25 30  
 agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca 144  
 Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr 45  
 35 40 45  
 cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg 192  
 Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser 60  
 50 55 60  
 gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg 240  
 Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro

| 65  | 70  | 75  |     |
|---|-----|-----|-----|
| gag gtc ccc cgg acg cgg cgt ccc gtt tcc ggg gcg gtt ttg tcc ggc |     |     | 288 |
| Glu Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly |     |     |     |
| 80  | 85  | 90  | 95  |
| ccg ggg cct gcg cgg gcg cct ccg cca ccc gct ggg tcc gga ggg gcc |     |     | 336 |
| Pro Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala |     |     |     |
|   | 100 | 105 | 110 |
| gga cgc aca ccc acc acc gcc ccc cgg gcc ccc cga acc cag cgg gtg |     |     | 384 |
| Gly Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val |     |     |     |
|   | 115 | 120 | 125 |
| gcg act aag gcc ccc gcg gcc ccg gcg gcg gag acc acc cgc ggc agg |     |     | 432 |
| Ala Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg |     |     |     |
|   | 130 | 135 | 140 |
| aaa tcg gcc cag cca gaa tcc gcc gca ctc cca gac gcc ccc gcg tcg |     |     | 480 |
| Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser |     |     |     |
|   | 145 | 150 | 155 |
| acg gcg cca acc cga tcc aag aca ccc gcg cag ggg ctg gcc aga aag |     |     | 528 |
| Thr Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys |     |     |     |
|   | 160 | 165 | 170 |
| ctg cac ttt agc acc gcc ccc cca aac ccc gac gcg cca tgg acc ccc |     |     | 576 |
| Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro |     |     |     |
|   | 180 | 185 | 190 |
| cgg gtg gcc ggc ttt aac aag cgc gtc ttc tgc gcc gcg gtc ggg cgc |     |     | 624 |
| Arg Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg |     |     |     |
|   | 195 | 200 | 205 |
| ctg gcg gcc atg cat gcc cgg atg gcg gcg gtc cag ctc tgg gac atg |     |     | 672 |
| Leu Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met |     |     |     |
|   | 210 | 215 | 220 |
| tcg cgt ccg cgc aca gac gaa gac ctc aac gaa ctc ctt ggc atc acc |     |     | 720 |
| Ser Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr |     |     |     |
|   | 225 | 230 | 235 |
| acc atc cgc gtg acg gtc tgc gag ggc aaa aac ctg ctt cag cgc gcc |     |     | 768 |
| Thr Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala |     |     |     |
|   | 240 | 245 | 250 |
| aac gag ttg gtg aat cca gac gtg gtg cag gac gtc gac gcg gcc acg |     |     | 816 |
| Asn Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr |     |     |     |
|   | 260 | 265 | 270 |
| gcg act cga ggg cgt tct gcg gcg tcg cgc ccc acc gag cga cct cga |     |     | 864 |
| Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg |     |     |     |
|   | 275 | 280 | 285 |
| gcc cca gcc cgc tcc gct tct cgc ccc aga cgg ccc gtc gag gaa ttc |     |     | 912 |
| Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe |     |     |     |

290

295

300

&lt;210&gt; 40

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: synthetic  
construct

&lt;400&gt; 40

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Arg | Arg | Ser | Val | Lys | Ser | Gly | Pro | Arg | Glu | Val | Pro | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Glu | Tyr | Glu | Asp | Leu | Tyr | Tyr | Thr | Pro | Ser | Ser | Gly | Met | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asp | Ser | Pro | Pro | Asp | Thr | Ser | Arg | Arg | Gly | Ala | Leu | Gln | Thr | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Gln | Arg | Gly | Glu | Val | Arg | Phe | Val | Gln | Tyr | Asp | Glu | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Leu | Tyr | Gly | Gly | Ser | Ser | Ser | Glu | Asp | Asp | Glu | His | Pro | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Arg | Thr | Arg | Arg | Pro | Val | Ser | Gly | Ala | Val | Leu | Ser | Gly | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ala | Arg | Ala | Pro | Pro | Pro | Pro | Ala | Gly | Ser | Gly | Gly | Ala | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Pro | Thr | Thr | Ala | Pro | Arg | Ala | Pro | Arg | Thr | Gln | Arg | Val | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Ala | Pro | Ala | Ala | Pro | Ala | Ala | Glu | Thr | Thr | Arg | Gly | Arg | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Gln | Pro | Glu | Ser | Ala | Ala | Leu | Pro | Asp | Ala | Pro | Ala | Ser | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Thr | Arg | Ser | Lys | Thr | Pro | Ala | Gln | Gly | Leu | Ala | Arg | Lys | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Phe | Ser | Thr | Ala | Pro | Pro | Asn | Pro | Asp | Ala | Pro | Trp | Thr | Pro | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Gly | Phe | Asn | Lys | Arg | Val | Phe | Cys | Ala | Ala | Val | Gly | Arg | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Met | His | Ala | Arg | Met | Ala | Ala | Val | Gln | Leu | Trp | Asp | Met | Ser |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Arg | Thr | Asp | Glu | Asp | Leu | Asn | Glu | Leu | Leu | Gly | Ile | Thr | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Arg | Val | Thr | Val | Cys | Glu | Gly | Lys | Asn | Leu | Leu | Gln | Arg | Ala | Asn |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



<210> 43  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 43  
aggaggtgga tctgc

15

<210> 44  
<211> 6  
<212> PRT  
<213> Mus musculus

<400> 44  
Glu Arg Met Arg Arg Pro  
1 5

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence

<400> 45  
Glu Arg Met Pro Pro Arg Arg Asp  
1 5

BI  
Conclude